Detection and Enumeration of Bacteria and Viruses of Extremophilic Tardigrades

Rhonda L. Lane

Department of Biological Sciences
Tennessee State University
3500 John A. Merritt Blvd, Nashville, Tennessee 37209
UNITED STATES OF AMERICA
rlane1@mytsu.tnstate.edu

Dr. Todd Gary

Center of Excellence in Information Systems
Tennessee State University
330 10th Avenue North, Nashville, Tennessee 37203
UNITED STATES OF AMERICA

Dr. E. Lewis Myles

Department of Biological Sciences Tennessee State University 3500 John A. Merritt Blvd, Nashville, Tennessee 37209 UNITED STATES OF AMERICA

Tardigrades (commonly known as water bears) are micrometazoans ranging in length from approximately 0.25 to 1.2 mm. They exhibit four pairs of clawed legs and fairly complex digestive and nervous systems. Tardigrades have been observed in almost every place on earth, from the Antarctic to the deep sea floor, as ubiquitous in extreme environments as many prokaryote extremophiles. Although there are over 800 known species surviving in most terrestrial and aquatic habitats, the study of this phylum has been relatively neglected. One unique characteristic of the small animals that has been studied is their ability to form a "tun" when environmental factors become unfavorable for survival. Due to their ubiquity and ability to live in extreme environments through tun formation, some scientists believe they are very ancient forms of animal life on Earth. Some even speculate that their ancestors migrated here from other planets. Unique phages of Archaebacteria such as those infecting Sulfolobus in hot springs have been identified recently in many extreme environments. The presence of bacterial and viral infestation has been documented anecdotally in Tardigrades with electron microscopy used for morphological studies of the Tardigrades themselves. This research will use size exclusion filtration and fluorescent staining to detect and enumerate the presence of bacteria and viruses infecting Tardigrades. In a later phase, identification will be confirmed through comparison to known sequences or documented as previously unknown through molecular, genetic and microscopic techniques.